



> stations.

>

> one issue with the replicate tox results for G786 and G788: one of the

> replicate results for 786 did not qualify as reference sample based on

> the criteria established, but the average of the results did qualify.

> In my treatment of the reference samples, I averaged the results for

> each of the control-normalized results for each endpoint for each of the

> two replicate pairs. I do not recall any specific guidance about

> treatment of replicates, but I recall raising the issue.

>

> I also support Bob's point about the best fit for 5th pctile, not

> necessarily the best overall fit. My recommendation is that EPA do the

> curve-fitting, determine the values, and provide a table of values to

> use for the thresholds. This would save all of us time and we could

> move on to more important issues (like what are we going to do with

> those values).

>

> Jay

>

> Robert Gensemer wrote:

>     Eric: A few observations from my perspective:

>

>     2) The control-normalization looks correct for biomass, but if I

>     recall (I don't have my files with me at the moment) that LWG's

>     biomass values for individual stations did not quite match values

>     that Jay derived for table RE-1.

>     3) You have the control normalization correct (test/control) but

>     we need to be careful to recommend use of survivorship, not

>     mortality, to be fully consistent with our guidance and numeric

>     examples. I realize Table 2-1 used mortality, but we have been

>     very consistent all along that we need to use survivorship, and

>     from a recent call with Burt, Don McD. agrees that

>     control-normalized survivorship is the correct value to use, not

>     ctrl-norm mortality. Yes, they relate directly (or should I say,

>     inversely) to one another, but the 5th percentile calculation

>     could be different using one vs. the other, so we need to be

>     consistent, and use survivorship.

>     4) I could not find any explicit guidance regarding the duplicate

>     RE samples. Its not in the McDonald report that I can find, and I

>     don't think we went into this level of detail in the problem

>     formulation. It may be one of those things that just seemed very

>     obvious to all of us, and so never felt the need to explicitly

>     direct it. Actually, it may have only come up, to my recollection,

>     during our own RE calculations in March. So table RE-1 definitely

>     reflects this approach, although I don't think it was spelled out

>     in the text.

>     6) I agree with your summary here, except to say that we need to

>     not just chose the best overall curve fit, but particularly in the

>     case of Hyalella biomass, we need a curve that fits the lower tail

>     (i.e., 5th %ile) of the distribution best. For the other three

>     endpoints, this is probably not an issue (i.e., best fit is also

>     best 5th %ile fit). But for Hyl biomass, we need to think more

>     carefully about what distribution fits at the lower tail of the

>     distribution. I think this is a valid approach that makes the best

>     out of the available data. LWG's curve fit created a 5th %ile

>     value that was quite a bit lower than the empirical numbers; I do

>     not think that was the most appropriate representation of the

>     data.

>

>     Bob

>

>     Parametrix 40th Anniversary, 1969-2009

>     inspired people . inspired solutions . making a difference

>

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>

>     p Before printing, please think green.

>

>

>     From: Blischke.Eric@epamail.epa.gov [Blischke.Eric@epamail.epa.gov

>     ]

>     Sent: Monday, July 13, 2009 5:02 PM

>     To: Robert Gensemer; Shephard.Burt@epamail.epa.gov;

>     jay.field@noaa.gov; Goulet.Joe@epamail.epa.gov

>     Cc: Humphrey.Chip@epamail.epa.gov

>     Subject: Summary of Sediment Bioassay Interpretation Resolution

>

>

>     As you are aware, we have been discussing some of the details of

>     the LWG's interpretation of the Portland Harbor sediment bioassay

>     results. Some elements of the interpretation were discussed

>     during a conference call on Thursday, June 18, 2009.

>

>     Here is where I believe we are:

>

>     1) No transcription errors were identified during a review of the

>     reference envelope bioassay results.

>     2) The total biomass calculations were done correctly.

>     3) Mortality should be computed as test/control. This is

>     consistent with Table 2-1 in the March 17, 2006 Bioassay

>     Interpretation Report, ASTM Method E-1706, and EPA Guidance.

>     4) Duplicate reference envelope samples should be pooled

>     (averaged) rather than treated as individual samples. This is

>     consistent with February 15, 2008 problem formulation (Note: is

> this the correct reference? I could not find this in either the  
> problem formulation nor the MacDonald benthic risk evaluation)  
> 5) Identification of Level 1, Level 2 and Level 3 thresholds:  
> The toxicity thresholds should be calculated based on 10% of the  
> reference envelope not an absolute 10%. This is consistent with  
> Tables RE 1, RE-2 and the text of EPA's March 31, 2009 direction  
> on the Calculation and Use of Reference Envelope for Portland  
> Harbor Sediment Toxicity Test Interpretation  
> 6) Identification of the 5% of the reference envelope should be  
> accomplished using a range of curve fitting procedures appropriate  
> for the data set distribution. The curve fitting procedure with  
> the best overall fit should be selected and the 5% calculated  
> using the best fit curve fitting procedure.  
>  
> The above procedures for computing the results of the bioassay  
> tests, calculating hit/no-hit designations, developing the  
> reference envelope and identifying Level 1, Level 2 and Level 3  
> toxicity hits should be followed.  
>  
> Please look this over and make sure it matches up with the  
> recommended procedures. See also my note about the pooling of the  
> reference duplicate samples. Once everyone agrees with the  
> outlined procedures, I will send an email to the LWG summarizing  
> this and recommending a conference call to discuss if there are  
> any questions.  
>  
> Thanks, Eric  
>  
> --  
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